

FIG.1

A

-156
-120 TTTAACTTTGAAGAATTTAAAAAACCATTAATTATATATTTATATAAATATATATATAAATCTGTATCCAGGCTGCTTATGAAGAAAGCTCATTAAAGAACAGTGGACCCAGGA
1 ATGGAATGCTCCACACCTTCTGGGTGGGCGCTGGACTTTGCTGCTCTTACGGGGATCTTGTGCTTTGTTGTTGCCCGGGAGTGGGTATTATCCAGGTTCTCTCAATCTTTTTC 40
M E L L H T F C G G R N T L L L F T G I L C F V V A R G V G Y Y P R F S P F F F

121 CTTTGCACTCATCGAGAAGTGAAGGAGATGGGAAACAGGAGAGTGTCTATCTCTGCACTGGCGGGCAACCCAGTACTACATACCTGGGCAGGAGTACATGTGACCATA 80
L C T H H G E L E G D G E Q G E V L I S L H L A G N P S Y Y I P G Q E Y H V T I

241 TCCACTAGTACCTTTCTTGATGGTCTTCTGGTACTGGACTTTACACTTCTACCACTGTTCAAGGCTCTCAGAGCATTGGAGGCTCTAAAGCATTGGATTGGTATTATGAGCGACCT 120
S T S A T F F D G L L V T G L Y T S T S V Q A S Q S I G G S K A F G F G I M S D R

361 CAGTTTGGTACCAGTTTATGTGAGTGTCTGTTCTCCACGTGAGTCATCTCCACAACAACTAAGTTTGTATGGATTGCACCACAGCAGGTACAGGATGTGCACTTCATG 160
Q F G T Q F M C S V V A S H V S H L P T T N L S F V W I A P P A G T G C V N F M

481 GCCACAGCAACACATAGGGACAAGTTATTTCAAGGATGCCCTGGCACAACATGTGCGAACAGGAGCTCTACTGAAGCTCCCTTGGGCTAATTTAGCCGAAATTCACAGTGAA 200
A T A T H R G Q V I F K D A L A Q Q L C E Q G A P T E A P L R P N L A E I H S E

601 AGCATCCTTTACGAGATGATTTTGACTCATATAAGCTTCAGGAATTGAATCCAAATATTTGGCTCAGTGCAGAAATGCGAAGTTGGTGAAGCAGTGTGGCAATTCATGATGGTGG 240
S I L L R D D F O S Y K L Q E L N P N I W L Q C R N C E V G E Q C G A I M H G G

721 GCAGTCACCTTTTGTGATCCGATGGACCAAGAGAATTGATAACTGTTCAAATGAACACAACACGTCATCTGTTTTCAGTCTTCTATTGGTCAAGGATCTGCGAGTTTCAGCTATTCA 280
A V T F C D P Y G P R E L I T V Q M N T T T A S V L Q F S I G S G S C R F S Y S

841 GACCTGGAAATTTGGTGTATACACAAAGAATAATTCATAGTGGATGCCATTGGAGAGAAATTAGTCTCTTCCAATGTTAGCACCATTACATTATTTACCTACCTCTGAA 320
D P G I V V S Y T K N N S S S W M P L E R I S A P S N V S T I I H I I Y L P P E

961 GCTAAAGGAGAAATGTGAATTCCTGGAGGAGAGAACATGCAAGGAGGTGATGTGATGAAGCTCTGCGGCACTGGATAACATTTTGATTATCAATGCTCTATAAAGAGTC 360
A K G E N V K F R H R Q E N M Q A G D V Y E A C H A L D N I L I I N A A H K E V

1081 GTGTTAGAAGCAATCTAGATCCAAATGGACACAGGAACTGGCTTTTTCCTGGGCTACTGTAAAGCATACTGTGAGTGGAACTCTATATATTTTCATGGTACAGAAAGC 400
V L E D N L D P M D T G N N W L F P A T K F C L X Q T S H R G H N L N V W A V D F V

1201 AGTGAATACAACCTTGTCTACTACAGAGATGTGGATCTTTCAGTGAGGACATCCAGGACCGTGGTCTGAAGAGTTTGAGAATCTACCACTGGTGGGAAATAGTTGGAGCAGTAATT 440
S E Y N F A T T R D V D L S S E D I Q D Q W S E E F E N L P A G W E I V G A V I

1321 GGAACAGAATGTGAACCATAGAAATCGGGTTCATCTCTGTTTGTGTTTGAAGGATGGAGAAAGAAAGTTTGCACCTTACATGGATACCAAGGATATGGGAACCTAAGGTTTATTTT 480
G T E C G T I E S G S S L V F L K D G E R K V C T P Y M D T T G Y G N L R F Y F

1441 ATCATGGGGGAATGTGAGTCCAGGAGATCTCATGAATATGTAATCTTTATGCTCAGATTGATGGTAGAAAGAGCATATTATTATGGATACCTTGTCTATTATCTTATAAG 520
I M G G M C S P G E S H E N D V I L Y A Q I D G R K E H I I M D T L A Y S S Y K

1561 GTTACTTCTCTGTTTCTGCTGTATAGTCTGATCTACAAACACCTGCTACTAAATTTTGTCTGAAGCAACAGTCACCGTGGTCATAACTTAAATGTTTGGGCTGGATTGTC 560
V T S L V S A V I S P D L Q T P A T K F C L X Q T S H R G H N L N V W A V D F V

1681 CATGTGCTACCTGATTTGCTTCACTGAATCACATATGGTTGAGTTTTCATTAACTTGGATGTGGTGGCAGCCTGGAACAGTGTGAGCCTGGAATTTTCTACAAATCATGGG 600
H V L P V L P S T E S H M V Q F S I N L G C G S H Q P G N S V S L E F S T N H G

1801 CGTAGTTGGTCTTTGTTGCACTCGGAGTGTCTCCAGAGCTATGTGGATCCCATCTACCGCAGCAGC-
R S W S L L H S E C L P E L C A G S H L P H S -

B

GGTAAATTTTAGATGTAGCCATGAGC 432
G

1321 ATTACATTTTATCAGTGAATGCAAGAAACAGTATTTATATACATATTTAAAGGTCAATACAGAACCTTAAATGGCAGGTTAGGGCTACCATGTAATATTTTATGTTTCATAA
1441 TGTATAGTGGTAAGTATTTACATAGCAGTACTGATTGATTATTTGTTGCTTTTACCCAGTTACAGCTAACACACAGGGCATTTTTTCCCAATGGCAACATCATTTTGGCCG
1561 TCTGAGCAGAACATTTGTTTATTTATGGCATTTGAACCTGTGCTATGAGAGTGCAGCTAAAATAAACTTCTGGCTATGGGTGTTACCATACAACTGGTACCTCATGACATAGAA
1681 AAATATGACTCACATTAATCAGTAAGATCAGTTCAAGTATAGTACGGTGCAATTAATCTGCCAATAAACATTTAGAATTTGATTTTATATTTTAAAGATTAGAATTGACTCCATT
1801 CTTGTACCTTGACATCATTTTGGCTAGTTTATGGGTCAATAGACAGCCATCATACATTAGTCAGAGTAAATCGAGCATTACAAAACCTCAATGAGCCATAGTGAGTGTGACATCAGAA
1921 GTGACTGTCAAGTAAATCAACATTTGCTCATACAGATGCACATTTGAACAGTGGATTCTTATCCAGAAAGGGCCATTTTACTATCACTCTGGGATTTAAATGCCACTTCAATTTGGA
2041 ACTTCAGGTCACAAAAATAGAATGGACATTTAAACATCATGTTCTCATTACCCCTAATAAACTCCGGTTTTTTT(A)

[illegible]

Xenopus 1: ME-LLHTFCGGRWTL LFTGIL CFVVARGVGYYPFSPFFFLCTHHGELEGDGEQGEVLI 59
mouse 1: RGCWAPRALVLAV LLATI RAR AT 58
human 1: RSGWARQTFLLA LGATI RAR AA 57

Xenopus 60: SLHLAGNPSYYITPGQYHVTISTSTFFDGLLVLTGLYTSTVMAQSISIGGSIAFGFGIMSD 119
mouse 59: I I M I S S 118
human 58: I I M I S 117

Xenopus 120: RQFGQFMCSVVASHVSHLPITNLSEFMIAPPAGTGCVNFMATATHRGQVIFKDALAQQL 179
mouse 119: H N 178
human 118: H N 177

Xenopus 180: CEQGAPTEAPLRPLNLAETHSEILLRDDFDYSKLQELNPNIWLQRCNCEMGEQCGAIMHG 239
mouse 179: TAYSH DVI QQL VE S M T 238
human 178: DVTVH H D I HQLO VE N T 237

Xenopus 240: GAVTFCDPYGPRELLITVQNTITASVLQFSIGSGSCRFSYSDPGLMSSYKNNSSSRMPD 299
mouse 239: N E T TCL S T A TAD IQ 298
human 238: N E T TGL S T L A AD IQ 297

Xenopus 300: ERISAPSNVSTILHITLPLPEAKGENVKPRWRDENMQADVVEACWALDNILITINAKHE 359
mouse 299: K R V L E S Q C K DSLRV E M S R 358
human 298: K R L E S Q C K LRV E S RQ 357

Xenopus 360: VVLELDLDMDTGNWLFPPGATVKHILUSDGNSIYFHGTSSEYVFATTRDVLSSSEDIQ 419
mouse 359: V S S NIG F T 418
human 358: S V S NIG F T 417

Xenopus 420: DWSEEFENLPAGWEIVGAVITTECGTILESGSLVFLRDGERRVCTPYMDTTGYGNLRFY 479
mouse 419: E SQ T D L V AD M L L S 478
human 418: E SQ T DVL L L M L S 477

Xenopus 480: FIMGGMLSPGESHENDVLYAKIDGRKEHIIIMOTLAYSSYKVTSLVSAVISPDQTATK 539
mouse 479: V I D M I K E AL T P M N E 538
human 478: V I D N I K E TL S P M N E 537

Xenopus 540: FCLKTSTRGHLNLVWAVDFVHLPVLPSTESHMDFISINLGGSHQPGNSVSLEFSTNH 599
mouse 539: R K Q M R F M I T 598
human 538: R IKN Q L R F M I T 597

Xenopus 600: GRSWSLCHSECLPELCAQSHLPHS 599
mouse 599: T I P 598
human 598: T I P 597



FIG.3

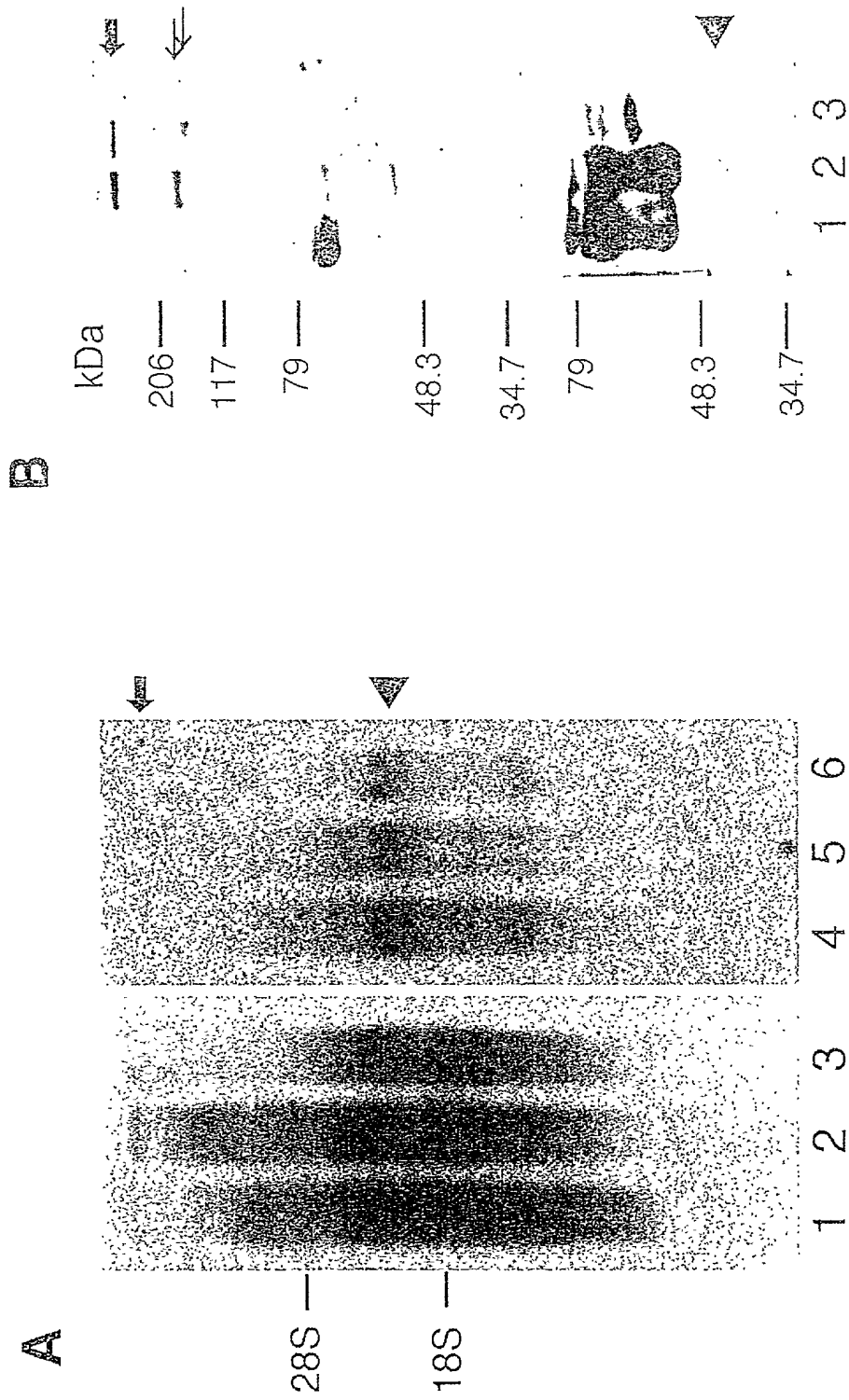


FIG.4

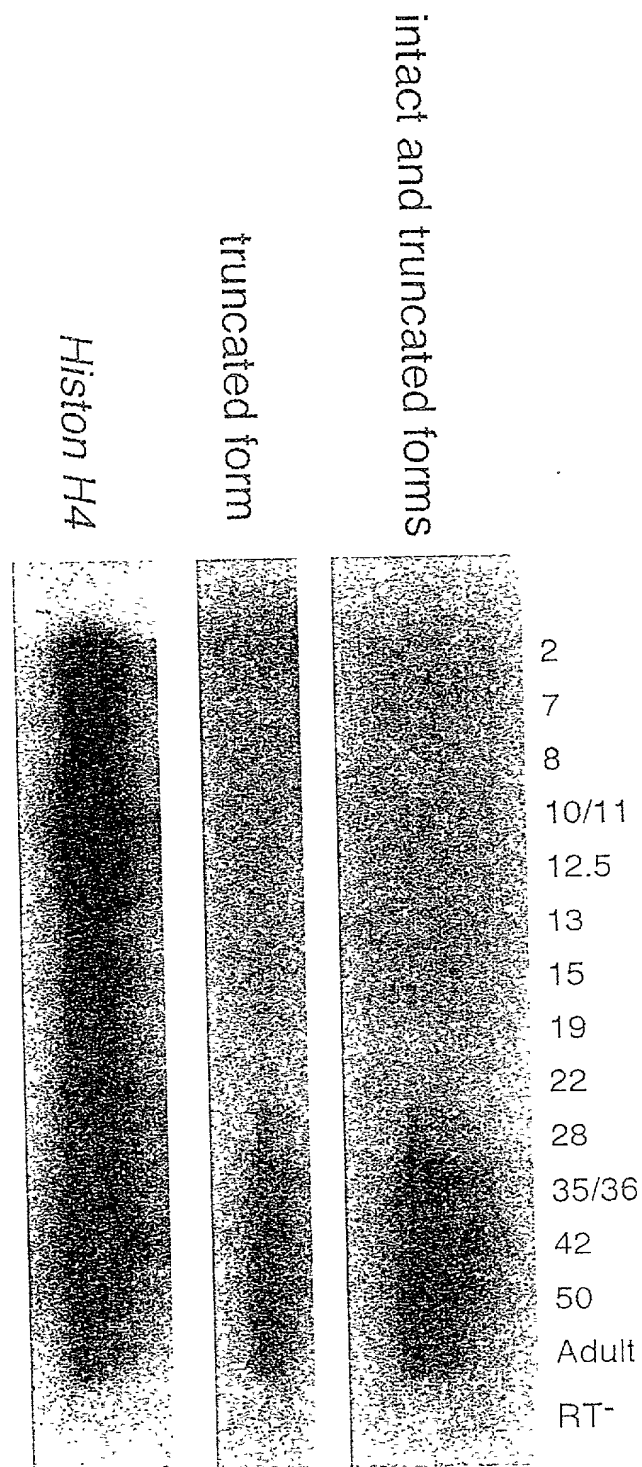


FIG.5

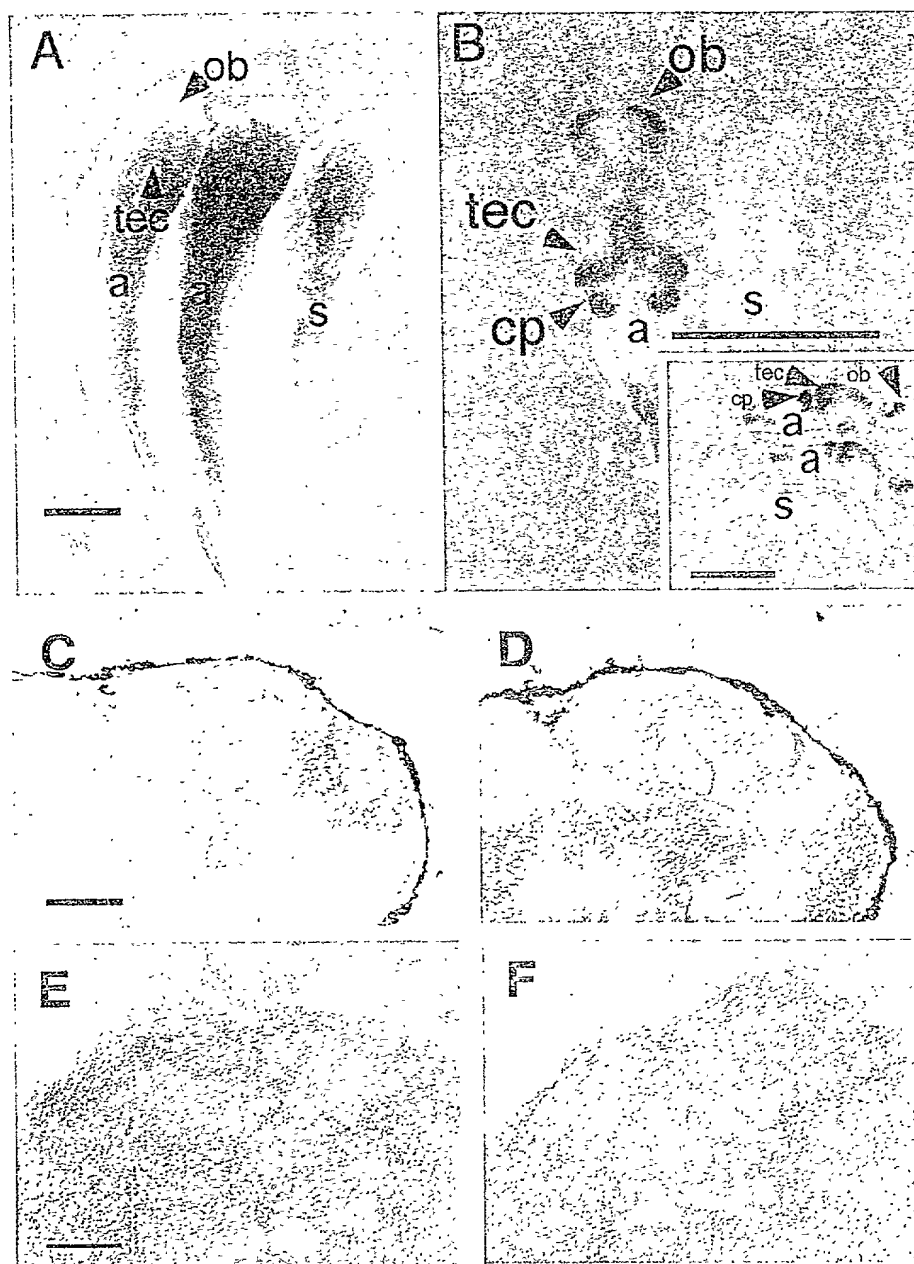


FIG.6

